



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 136085

TO: Sarvamangala Devi
Art Unit: 1645
Location: REM 3C18
Serial Number: 09/964858

Friday, June 10, 2005

From: Beverly Shears
Location: Biotech-Chem Library
REM 1A54
Phone: 571-272-2528
beverly.shears@uspto.gov

Search Notes

Protein Sequence Searches – February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (uniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

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OM protein - protein search, using sw model

Run on: June 8, 2005, 15:52:15, Search time 162 seconds

(without alignments)
627.889 Million cell updates/sec

Title: US-09-964-858a-1_COPY_1_263
Perfect score: 1386
Sequence: 1 MNSTPSKLLPDKSHSLQ.....NNNEVNSEPALTMKLR 263

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003s:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1386	100.0	1664	AAW99462	AAW99462 C.albican
2	1386	100.0	1664	AAE19799	AAE19799 Candida a
3	1386	100.0	1664	AAU79331	AAU79331 Candida a
4	1386	100.0	1664	ADC73265	ADC73265 Yeast Int
5	1378	99.4	1664	ADM33264	ADM33264 Candida a
6	241	17.4	236	AAW99456	AAW99456 Amino aci
7	241	17.4	236	AAE19800	AAE19800 Candida a
8	241	17.4	236	ADM33265	ADM33265 Candida a
9	139.5	10.1	1166	ABJ18982	ABJ18982 Pathogen
10	138.5	10.0	1166	AAW08643	AAW08643 S. aureus
11	137.5	9.9	371	ABG93277	ABG93277 C. albica
12	134.5	9.7	1133	AAE35697	AAE35697 Human Mas
13	134.5	9.7	1133	ADC59316	ADC59316 Human pol
14	134.5	9.7	1133	ABU05434	ABU05434 Human bre
15	134	9.7	1141	ABU42327	ABU42327 Protein e
16	133	9.6	767	ABBS8240	ABBS8240 Drosophi
17	133	9.6	971	AAW48896	AAW48896 Candida a
18	131.5	9.5	1174	AAE85039	AAE85039 Shrimp wh
19	131.5	9.5	2439	ABE68896	ABE68896 Drosophi
20	128	9.2	618	ADL33450	ADL33450 Lolium pe
21	127.5	9.2	1335	ABP38871	ABP38871 Staphyloc
22	127.5	9.2	1335	ABJ19029	ABJ19029 Pathogen
23	127.5	9.2	1335	ADSO6472	ADSO6472 Staphyloc
24	127.5	9.2	1542	ABB71456	ABB71456 Drosophi
25	127	9.2	4134	AAJ31946	AAJ31946 Plaemodiu

26	126	9.1	1817	3	ABA42230	Abb42230 Human ORF
27	125	9.0	722	4	ABE63899	Abb63899 Drosophi
28	125	9.0	1545	4	ABE65577	Abb65577 Drosophi
29	124.5	9.0	811	4	ABE62661	Abb62661 Drosophi
30	124	8.9	1798	4	ABE71695	Abb71695 Drosophi
31	124	8.9	2781	3	AAE57453	AAE57453 Human tra
32	124	8.9	2781	8	ADP42724	AdP42724 Human BPT
33	124	8.9	2781	8	ADQ18653	AdQ18653 Human Bof
34	123	8.9	672	4	AAW93543	AAW93543 Human pol
35	123	8.9	672	8	ADL31262	ADL31262 Human pro
36	123	8.9	874	4	ABE62601	ABE62601 Drosophi
37	123	8.9	1080	5	ABG93254	ABG93254 C. albica
38	123	8.9	1139	6	ABU35640	ABU35640 Protein e
39	123	8.9	1139	7	ABO23514	ABO23514 Mycoplasma
40	123	8.9	1557	4	ABE63735	Abb63735 Drosophi
41	123	8.9	1616	6	ABU35669	ABU35669 Protein e
42	123	8.9	1616	6	ABO23515	ABO23515 Mycoplasma
43	123	8.9	4019	4	AAE13839	AAE13839 Human lun
44	123	8.9	4019	7	ADP66733	AdP66733 Human lun
45	123	8.9	4019	7	ADP67987	AdP67987 Human lun

ALIGNMENTS

RESULT 1
ID AAW99462 standard; protein, 1664 AA.

AAW99462;

08-JUN-1999 (first entry)

C.albicans alpha-INT1p protein.

Integrin-like motif; vaccine; immune response; antibody; inhibition;
adhesion; endothelial cell; pathogenesis; infection; probe.

Candida albicans.

US586151-A.

23-MAR-1999.

03-MAY-1996; 96US-00642846.

03-MAY-1996; 96US-00642846.

(MINT) UNIV MINNESOTA.

Tao N, Kendrick K, Gale CA, Hostetter MK, Bendel CM,

WPI; 1999-242618/20.

N-PSDB; AAX5885.

New isolated Candida albicans protein with integrin-like motifs.

Example; Col 13-14; 21pp; English.

This sequence represents the Candida albicans alpha-INT1 protein which contains integrin-like motifs. The protein was used to derive peptides AAW99456-W99461 used for producing vaccines for stimulating an immune response. The antibodies can inhibit the adhesion of C.albicans to cells, particularly endothelial cells. This blocking activity of the adhesion to cells can reduce or prevent subsequent events in the pathogenesis of invasive candidal infection

Sequence 1664 AA;

Query Match 100.0%; Score 1386; DB 2; Length 1664;
Best Local Similarity 100.0%; Pred. No. 9.3e-107;
Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OM protein - protein search, using sw model

Run on: June 8, 2005, 16:21:02 / Search time 173 Seconds
(without alignments)
778.479 Million cell updates/sec

Title: US-09-964-858A-1_COPY_1_263

Perfect score: 263
Sequence: 1 MNSYPSKLPIDKSHSLQ.....KNNNEVNSPALTMKLR 263

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size: 0

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 1000 summaries

Database: Uniprot_03.*

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	263	100.0	1664	1 INT1 CANAL	P53705 candida alb
2	11	4.2	840	2 O6CHB0	O6chb0 yarrowia li
3	11	4.2	2123	2 O9U987	O9u987 dictyostell
4	11	4.2	2189	2 O7SB06	O7sbu6 dictyostell
5	10	3.8	31	2 O64LJ3	O64lj3 pongo pygma
6	10	3.8	58	2 O9V8P4	O9v8f4 dictyostell
7	10	3.8	210	2 O86127	O86127 dictyostell
8	10	3.8	224	2 O7PRM3	O7prk3 anophelae g
9	10	3.8	225	2 O9C1A4	O9c1a4 trichophyto
10	10	3.8	247	2 O86YX1	O86y1 dictyostell
11	10	3.8	255	1 LPE1 SIMTR	P15714 elmeria ten
12	10	3.8	271	2 O7PEH6	O7peh6 anophelae g
13	10	3.8	279	2 O35846	O35846 mus musculu
14	10	3.8	286	1 MCM1 YEAST	P11746 saccharomyc
15	10	3.8	320	2 O7SG91	O7sg91 dictyostell
16	10	3.8	333	2 O9W0N1	O9w0n1 dictyostell
17	10	3.8	337	2 O6VT44	O6vt44 vibrio para
18	10	3.8	353	2 O6VXK6	O6vix6 dictyostell
19	10	3.8	355	2 O6VXK6	O6vix6 dictyostell
20	10	3.8	359	2 O9UAF7	O9uaf7 branchiosto
21	10	3.8	360	2 O77158	O77158 branchiosto
22	10	3.8	362	2 O64OM3	O64om3 mus musculu
23	10	3.8	363	1 TOB1 MOUSE	O64f71 mus musculu
24	10	3.8	373	2 O6CFI0	O6cfi0 yarrowia li
25	10	3.8	411	2 O8MU88	O8mu88 strongyloce
26	10	3.8	443	2 O86NLS	O86nls dictyostell
27	10	3.8	447	2 O7PQ39	O7pq39 anophelae g
28	10	3.8	448	1 AAC2 DICDI	P14196 dictyostell
29	10	3.8	464	2 O6H971	O6h971 antirrhinum
30	10	3.8	486	2 O6CDX5	O6cdx5 yarrowia li
31	10	3.8	490	2 O811G0	O811g0 dictyostell

32	10	3.8	536	2 O9P466	O9p466 neurospora
33	10	3.8	550	1 CCF DROME	P41046 dictyostell
34	10	3.8	550	2 O9VNT6	O9vnt6 dictyostell
35	10	3.8	555	2 O869R1	O869r1 dictyostell
36	10	3.8	572	2 O95BN1	O95bn1 dictyostell
37	10	3.8	578	2 O86P22	O86p22 dictyostell
38	10	3.8	581	2 O18349	O18349 dictyostell
39	10	3.8	582	2 O9VUH2	O9vuh2 dictyostell
40	10	3.8	609	2 O7KSW2	O7ksw2 dictyostell
41	10	3.8	622	2 O7SAK7	O7sak7 neurospora
42	10	3.8	628	2 O9VSB3	O9vsb3 dictyostell
43	10	3.8	639	2 O7SHN2	O7shn2 neurospora
44	10	3.8	648	1 KAPC DICDI	P34039 dictyostell
45	10	3.8	648	2 O9TXB8	O9txb8 dictyostell
46	10	3.8	661	2 O960R6	O960r6 dictyostell
47	10	3.8	662	2 O780R1	O780r1 neurospora
48	10	3.8	675	2 O9Y110	O9y110 dictyostell
49	10	3.8	682	2 O86K87	O86k87 dictyostell
50	10	3.8	707	2 O00910	O00910 dictyostell
51	10	3.8	716	2 O7KRB6	O7krb6 dictyostell
52	10	3.8	717	1 ARA DROME	O24248 dictyostell
53	10	3.8	724	2 O86B89	O86b89 anophelae g
54	10	3.8	738	2 O06628	O06628 saccharomyc
55	10	3.8	745	2 O8X0W4	O8x0w4 neurospora
56	10	3.8	756	2 O86PD9	O86pd9 dictyostell
57	10	3.8	759	2 O9VK09	O9vk09 dictyostell
58	10	3.8	772	2 O86P40	O86p40 dictyostell
59	10	3.8	789	2 O86AC9	O86ac9 dictyostell
60	10	3.8	791	1 CUDA DICDI	O00841 dictyostell
61	10	3.8	796	2 O7JF60	O7jfp0 dictyostell
62	10	3.8	796	2 O9V7U9	O9v7u9 dictyostell
63	10	3.8	797	2 O7KRE3	O7kre3 dictyostell
64	10	3.8	800	2 O91551	O91551 xenopus lae
65	10	3.8	806	2 O96828	O96828 dictyostell
66	10	3.8	812	2 O75J16	O75j16 dictyostell
67	10	3.8	815	2 O80XQ2	O80xq2 mus musculu
68	10	3.8	816	2 O86HD8	O86hd8 dictyostell
69	10	3.8	833	2 O76P07	O76p07 dictyostell
70	10	3.8	836	2 O784H0	O784h0 neurospora
71	10	3.8	836	2 O81P74	O81p74 dictyostell
72	10	3.8	836	2 O8MCP0	O8mcp0 dictyostell
73	10	3.8	837	2 O86NTO	O86nt0 dictyostell
74	10	3.8	854	2 O801P6	O801p6 xenopus lae
75	10	3.8	865	2 O91YX8	O91yx8 spalax juda
76	10	3.8	865	2 O91YB0	O91yb0 spalax galli
77	10	3.8	865	2 O91YB2	O91yb2 spalax carm
78	10	3.8	878	2 O81NR4	O81nr4 dictyostell
79	10	3.8	889	2 O8MLW9	O8mlw9 dictyostell
80	10	3.8	893	2 O8MNS5	O8mns5 dictyostell
81	10	3.8	916	2 O6CF23	O6cf23 yarrowia li
82	10	3.8	926	2 O9W3G1	O9w3g1 dictyostell
83	10	3.8	926	2 O81P76	O81p76 dictyostell
84	10	3.8	926	2 O9W3G1	O9w3g1 dictyostell
85	10	3.8	979	2 O7KWS3	O7kws3 dictyostell
86	10	3.8	981	2 O8M011	O8m011 dictyostell
87	10	3.8	993	2 O7SD03	O7sd03 neurospora
88	10	3.8	1019	2 O6Z523	O6z523 homo sapien
89	10	3.8	1024	2 O6PJG2	O6pjg2 homo sapien
90	10	3.8	1024	2 O6PK13	O6pk13 homo sapien
91	10	3.8	1024	2 O86BG2	O86bg2 dictyostell
92	10	3.8	1036	2 O6PKS9	O6pks9 homo sapien
93	10	3.8	1080	1 HDC DROME	O9znp6 dictyostell
94	10	3.8	1180	2 O7JF26	O7jfp6 dictyostell
95	10	3.8	1186	2 O9VBD3	O9vbd3 dictyostell
96	10	3.8	1206	1 BUN2 DROME	O9ved3 dictyostell
97	10	3.8	1208	2 O86HFS	O86hfs dictyostell
98	10	3.8	1230	2 O9GUS3	O9gus3 dictyostell
99	10	3.8	1260	2 O9U919	O9u919 homo sapien
100	10	3.8	1271	2 O86123	O86123 dictyostell
101	10	3.8	1319	2 NNI HUMAN	O10571 homo sapien
102	10	3.8	1324	2 O6C0X9	O6c0x9 kluyveromyc
103	10	3.8	1358	2 O7RW22	O7rw22 neurospora
104	10	3.8	1368	1 SUT2 DROME	P25172 dictyostell
				2 O9V6J0	O9v6j0 dictyostell

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OM protein - protein search, using sw model

Run on: June 8, 2005, 16:12:52 ; Search time 41 seconds
(without alignments)
617.195 Million cell updates/sec

Title: US-09-964-858a-1_COPY_1_263
Perfect score: 263
Sequence: 1 NMSTPSKLLPIDKSHLQD.....NNKNVNSPRLTDKLR 263

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database : PIR 79: *
1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	263	100.0	1664	2 T18216	integrin-like prot
2	10	3.8	255	2 A60637	mezozone antigen
3	10	3.8	286	2 A34599	DNA-binding protei
4	10	3.8	448	2 S05355	hypothetical prote
5	10	3.8	648	1 JQ1150	protein kinase (BC
6	10	3.8	738	2 S59842	probable membrane
7	10	3.8	800	2 T51653	derRNA-binding prot
8	10	3.8	806	2 T13690	hypothetical prote
9	10	3.8	1180	2 S69205	stripe a/b protein
10	10	3.8	1212	2 T13804	shs protein - fruit
11	10	3.8	1365	2 S14871	suppressor two of
12	10	3.8	1390	2 T14004	trif protein - all
13	10	3.8	1655	2 T13998	gene maternind pr
14	10	3.8	2715	2 T13049	eyelid - fruit fly
15	10	3.4	104	2 T29540	hypothetical prote
16	9	3.4	154	2 T06508	glutinin low molec
17	9	3.4	473	2 T09580	hypothetical prote
18	9	3.4	488	2 A55180	homeotic protein H
19	9	3.4	597	2 T51889	related to clathri
20	9	3.4	644	2 S39356	transcription fact
21	9	3.4	760	2 A45174	eye cell developm
22	9	3.4	846	2 S57580	penicillin-binding
23	9	3.4	1026	2 T20369	hypothetical prote
24	9	3.4	1048	2 T31425	C-terminal domain
25	9	3.4	1271	2 T24008	hypothetical prote
26	9	3.4	1893	2 A56158	eye development pr
27	8	3.0	268	2 T04966	hypothetical prote
28	8	3.0	288	2 T06662	hypothetical prote
29	8	3.0	303	2 T06981	low-molecular-weig

30	8	3.0	304	2 T06505	glutinin low molec
31	8	3.0	323	2 T06506	glutinin low molec
32	8	3.0	355	2 T24010	hypothetical prote
33	8	3.0	394	2 S26492	homeotic protein A
34	8	3.0	399	2 T24031	probable guanine n
35	8	3.0	411	2 T29475	hypothetical prote
36	8	3.0	428	2 F96782	hypothetical prote
37	8	3.0	444	2 A43481	CCAAT/enhancer-bin
38	8	3.0	476	2 A39621	homeotic protein H
39	8	3.0	484	2 S44739	CO2C2.1 protein -
40	8	3.0	534	2 T15141	hypothetical prote
41	8	3.0	551	2 F70684	hypothetical prote
42	8	3.0	551	2 S66701	probable membrane
43	8	3.0	592	2 T21536	hypothetical prote
44	8	3.0	613	2 S48557	hypothetical prote
45	8	3.0	625	2 T50992	hypothetical prote
46	8	3.0	632	2 T48316	hypothetical prote
47	8	3.0	643	2 S55610	polypeptide - equi
48	8	3.0	654	2 T30136	hypothetical prote
49	8	3.0	684	2 A56154	Abi substrate ena
50	8	3.0	730	2 A75486	hypothetical prote
51	8	3.0	738	2 S37876	glutamine-rich pro
52	8	3.0	779	2 T20654	hypothetical prote
53	8	3.0	788	2 T25061	hypothetical prote
54	8	3.0	806	2 S22765	heterogeneous ribo
55	8	3.0	873	2 S53225	ecdysone-induced p
56	8	3.0	875	1 UW0106	3',5'-cyclic-GMP p
57	8	3.0	904	2 G64840	protein-histidine
58	8	3.0	933	2 F86427	auxin response fac
59	8	3.0	992	2 A42318	glycogen phosphory
60	8	3.0	1004	2 H88562	protein C07A5.3 [I
61	8	3.0	1044	2 S40704	hypothetical prote
62	8	3.0	1088	2 H86747	unknown protein T1
63	8	3.0	1102	2 T39943	hypothetical prote
64	8	3.0	1198	2 T49726	hypothetical prote
65	8	3.0	1209	2 T31353	brachma associated
66	8	3.0	1237	2 A34598	ecdysone-induced p
67	8	3.0	1314	1 TMBYR6	transcription regu
68	8	3.0	1480	2 S48440	poly(A)-specific r
69	8	3.0	1558	2 C89114	protein C37C3.6a [
70	8	3.0	1572	2 S45251	SNR2a1pha protein
71	8	3.0	1596	2 A33106	neurogenic locus m
72	8	3.0	2027	2 S60123	hypothetical prote
73	8	3.0	2056	2 G88564	protein R10E1.1 [
74	8	3.0	2167	2 T34395	hypothetical prote
75	8	2.7	111	2 B30102	GTP-binding protei
76	7	2.7	110	2 T49553	hypothetical prote
77	7	2.7	120	2 G82653	HCB-related prote
78	7	2.7	125	2 S80762	probable regulator
79	7	2.7	132	2 P85635	hypothetical prote
80	7	2.7	172	1 D31482	H+-transporting tw
81	7	2.7	183	2 D90335	terminal quinol ox
82	7	2.7	206	2 S44894	ZK1236.6 protein -
83	7	2.7	206	2 S61705	hypothetical prote
84	7	2.7	207	2 S32124	B2 protein - carro
85	7	2.7	213	2 T23865	hypothetical prote
86	7	2.7	223	2 S16269	auxin-induced prote
87	7	2.7	229	2 S16268	glutinin low molec
88	7	2.7	229	2 S7654	glutinin low molec
89	7	2.7	234	2 D96592	hypothetical prote
90	7	2.7	239	2 C88395	protein P53A3.4 [I
91	7	2.7	243	2 T27493	hypothetical prote
92	7	2.7	244	2 S07398	gamma-Gliadin B pr
93	7	2.7	250	2 C86429	hypothetical prote
94	7	2.7	261	2 UN0747	histone H1-I - Vol
95	7	2.7	261	2 S57655	glutinin low molec
96	7	2.7	267	1 S30863	BMI1 protein - yea
97	7	2.7	267	2 T15645	hypothetical prote
98	7	2.7	276	2 S57656	glutinin low molec
99	7	2.7	281	2 JC2495	heat-shock protein
100	7	2.7	285	2 S20853	glutinin low molec
101	7	2.7	286	2 T05910	glutinin low molec
102	7	2.7	295	1 UN0696	glutinin low molec

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OW protein - protein search, using SW model

Run on: June 8, 2005, 16:28:54 / Search time 157 Seconds
(without alignments)
642.146 Million cell updates/sec

Title: US-09-964-858a-1_COPY_1_263

Perfect score: 263

Sequence: 1 MNSTPSKLPIIDKSHLQLQ.....NKNNEVSEPALTDMLKR 263

Scoring table: OLIGO

Gapop 60.0, Gapext 60.0

Searched: 1710399 seqs, 38333425 residues

Word size: 0

Total number of hits satisfying chosen parameters: 1710399

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	263	100.0	1664	10	US-09-978-343-2
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6	10	3.8	9	16	US-10-856-499-653
7	10	3.8	181	15	US-10-424-599-159517
8	10	3.8	286	9	US-09-801-368-188
9	10	3.8	286	15	US-10-451-467A-306
10	10	3.8	295	15	US-10-424-599-272882
11	10	3.8	406	15	US-10-369-493-3147

12	10	3.8	427	16	US-10-425-115-258112	Sequence 258112, A
13	10	3.8	648	17	US-10-732-923-10742	Sequence 10742, A
14	10	3.8	743	14	US-10-278-703-4	Sequence 4, Appl1
15	10	3.8	743	15	US-10-380-334-4	Sequence 4, Appl1
16	10	3.8	797	14	US-10-032-585-7208	Sequence 7208, Ap
17	10	3.8	920	13	US-10-087-192-1518	Sequence 1518, Ap
18	10	3.8	1038	9	US-09-752-639-151	Sequence 151, App
19	10	3.8	1038	9	US-09-984-198-151	Sequence 151, App
20	10	3.8	1038	17	US-10-967-092-151	Sequence 151, App
21	10	3.8	1319	16	US-10-732-923-13758	Sequence 2204, Ap
22	10	3.8	1358	16	US-10-778-804-11	Sequence 11, Appl
23	10	3.8	1692	15	US-10-432-422-41	Sequence 41, Appl
24	9	3.4	149	16	US-10-425-115-349865	Sequence 349865, A
25	9	3.4	265	9	US-09-960-253-185	Sequence 185, App
26	9	3.4	275	15	US-10-424-599-184082	Sequence 184082, A
27	9	3.4	307	15	US-10-732-923-18899	Sequence 8899, Ap
28	9	3.4	328	15	US-10-424-599-203656	Sequence 203656, A
29	9	3.4	345	9	US-09-843-846-2	Sequence 2, Appl1
30	9	3.4	345	16	US-10-648-599-210	Sequence 210, App
31	9	3.4	345	16	US-10-739-043-2	Sequence 2, Appl1
32	9	3.4	351	15	US-10-334-143-53	Sequence 53, Appl
33	9	3.4	353	9	US-09-925-297-814	Sequence 814, App
34	9	3.4	503	15	US-10-424-599-211275	Sequence 211275, A
35	9	3.4	548	16	US-10-767-701-44506	Sequence 44506, A
36	9	3.4	568	17	US-10-732-923-13759	Sequence 13759, A
37	9	3.4	580	17	US-10-732-923-13758	Sequence 13758, A
38	9	3.4	586	16	US-10-425-115-327159	Sequence 327159, A
39	9	3.4	712	17	US-10-732-923-17486	Sequence 17486, A
40	9	3.4	717	15	US-10-425-114-66724	Sequence 66724, A
41	9	3.4	752	13	US-10-108-605-133	Sequence 133, App
42	9	3.4	752	14	US-10-190-012-29	Sequence 29, Appl
43	9	3.4	752	17	US-10-689-576-29	Sequence 29, Appl
44	9	3.4	760	8	US-08-754-118-2	Sequence 2, Appl1
45	9	3.4	769	16	US-10-415-965-181417	Sequence 181417, A
46	9	3.4	1026	17	US-10-415-965-2	Sequence 2, Appl1
47	9	3.4	1257	17	US-10-741-849-7141	Sequence 7141, Ap
48	9	3.4	1736	16	US-10-437-963-188684	Sequence 188684, A
49	9	3.4	2017	15	US-10-114-270-86	Sequence 86, Appl
50	8	3.0	44	9	US-09-864-761-40491	Sequence 4491, A
51	8	3.0	80	16	US-10-425-115-260679	Sequence 260679, A
52	8	3.0	87	15	US-10-424-599-166633	Sequence 166633, A
53	8	3.0	93	15	US-10-424-599-222192	Sequence 222192, A
54	8	3.0	94	16	US-10-425-115-215073	Sequence 215073, A
55	8	3.0	102	15	US-10-424-599-201710	Sequence 201710, A
56	8	3.0	105	9	US-09-738-626-5146	Sequence 5146, Ap
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58	8	3.0	145	16	US-10-425-115-352152	Sequence 352152, A
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63	8	3.0	189	16	US-10-739-930-8830	Sequence 8830, Ap
64	8	3.0	208	9	US-09-864-761-36456	Sequence 36456, A
65	8	3.0	219	15	US-10-094-749-2381	Sequence 2381, Ap
66	8	3.0	275	15	US-10-425-114-38594	Sequence 38594, A
67	8	3.0	292	16	US-10-451-467A-436	Sequence 436, App
68	8	3.0	300	16	US-10-424-599-186521	Sequence 186521, A
69	8	3.0	303	16	US-10-437-963-116439	Sequence 116439, A
70	8	3.0	304	16	US-10-739-930-9778	Sequence 9778, Ap
71	8	3.0	310	16	US-10-821-273-80	Sequence 80, Appl
72	8	3.0	313	17	US-10-774-355A-1568	Sequence 1568, Ap
73	8	3.0	341	16	US-10-739-930-9636	Sequence 9636, Ap
74	8	3.0	346	16	US-10-732-923-134252	Sequence 134252, A
75	8	3.0	348	16	US-10-424-599-159122	Sequence 159122, A
76	8	3.0	348	15	US-10-425-114-37391	Sequence 37391, A
77	8	3.0	355	16	US-10-469-483-2	Sequence 2, Appl1
78	8	3.0	378	9	US-09-970-711-6	Sequence 6, Appl1
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84	8	3.0	594	15	US-10-425-114-70186	Sequence 70186, A

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OM protein - protein search, using sw model

Run on: June 8, 2005, 16:28:19 ; Search time 42 Seconds

(without alignments)
467,445 Million cell updates/sec

Title: US-09-964-858A-1_COPY_1_263

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Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Word size : 0

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Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	263	100.0	1664	4 US-09-978-943-2	Sequence 2, Appl1
5	72	27.4	927	4 US-09-248-796A-14284	Sequence 14284, A
6	46	17.5	236	1 US-09-599-652-3	Sequence 3, Appl1
7	46	17.5	236	2 US-08-642-846-3	Sequence 3, Appl1
8	46	17.5	236	3 US-09-264-604-3	Sequence 3, Appl1
9	46	17.5	236	4 US-09-978-943-3	Sequence 3, Appl1
10	10	3.8	86	4 US-09-248-796A-21968	Sequence 21968, A
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12	10	3.8	239	4 US-09-248-796A-15289	Sequence 15289, A
13	10	3.8	233	4 US-09-248-796A-27017	Sequence 27017, A
14	10	3.8	236	4 US-09-248-796A-19181	Sequence 19181, A
15	10	3.8	232	4 US-09-248-796A-24866	Sequence 24866, A
16	10	3.8	332	4 US-09-248-796A-23546	Sequence 23546, A
17	10	3.8	448	4 US-09-248-796A-18659	Sequence 18659, A
18	10	3.8	738	4 US-09-538-092-818	Sequence 818, App
19	10	3.8	1038	4 US-09-081-385-151	Sequence 151, App
20	10	3.8	1319	4 US-09-538-092-1291	Sequence 1291, App
21	10	3.8	1343	4 US-09-949-016-10641	Sequence 10641, A
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53	8	3.0	712	4 US-09-248-796A-19645	Sequence 19645, A
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55	8	3.0	806	1 US-07-980-528-2	Sequence 2, Appl1
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60	8	3.0	855	4 US-09-618-425-11	Sequence 11, Appl1
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62	8	3.0	875	1 US-08-250-8478B-23	Sequence 23, Appl1
63	8	3.0	875	2 US-08-463-949A-23	Sequence 23, Appl1
64	8	3.0	875	2 US-08-464-410A-23	Sequence 23, Appl1
65	8	3.0	875	3 US-09-226-741-5	Sequence 5, Appl1
66	8	3.0	875	4 US-09-595-514-5	Sequence 5, Appl1
67	8	3.0	875	5 PCT-US94-06066-23	Sequence 23, Appl1
68	8	3.0	928	4 US-09-506-066B-2	Sequence 2, Appl1
69	8	3.0	945	4 US-09-248-796A-15743	Sequence 15743, A
70	8	3.0	1357	4 US-09-270-767-44971	Sequence 44971, A
71	7	2.7	65	4 US-09-248-796A-23338	Sequence 23338, A
72	7	2.7	65	4 US-09-248-796A-23824	Sequence 23824, A
73	7	2.7	91	4 US-09-248-796A-26462	Sequence 26462, A
74	7	2.7	91	4 US-09-270-767-35416	Sequence 35416, A
75	7	2.7	91	4 US-09-270-767-35438	Sequence 35438, A
76	7	2.7	106	4 US-09-270-767-35438	Sequence 35438, A
77	7	2.7	106	4 US-09-270-767-51655	Sequence 51655, A
78	7	2.7	107	4 US-09-248-796A-16188	Sequence 26188, A
79	7	2.7	110	4 US-09-538-092-468	Sequence 468, App
80	7	2.7	126	4 US-09-248-796A-23808	Sequence 23808, A
81	7	2.7	132	3 US-09-224-505-5	Sequence 5, Appl1
82	7	2.7	132	3 US-09-224-505-6	Sequence 6, Appl1
83	7	2.7	135	4 US-09-270-767-34885	Sequence 34885, A
84	7	2.7	135	4 US-09-270-767-50102	Sequence 50102, A
85	7	2.7	138	4 US-09-270-767-31670	Sequence 31670, A
86	7	2.7	138	4 US-09-270-767-52887	Sequence 52887, A
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88	7	2.7	139	4 US-09-248-796A-18815	Sequence 18815, A
89	7	2.7	141	4 US-09-270-767-38716	Sequence 38716, A
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92	7	2.7	152	4 US-09-270-767-55991	Sequence 54991, A
93	7	2.7	154	4 US-09-248-796A-21018	Sequence 21018, A
94	7	2.7	159	4 US-09-248-796A-21018	Sequence 19024, A
95	7	2.7	176	4 US-09-248-796A-23424	Sequence 23424, A
96	7	2.7	189	4 US-09-270-767-43574	Sequence 43574, A
97	7	2.7	201	4 US-09-252-991A-29221	Sequence 29221, A
98	7	2.7	205	3 US-09-080-983-19	Sequence 19, Appl1
99	7	2.7	205	3 US-08-630-915A-16	Sequence 16, Appl1
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OM protein - protein search, using sw model

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(without alignments)
1356.240 Million cell updates/sec

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Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARYS

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5	87	33.1	1664	7 ADM33264	ADM33264 Candida a
6	46	17.5	236	2 AAW99456	AAW99456 Amino aci
7	46	17.5	236	5 AAH19800	AAH19800 Candida a
8	46	17.5	236	5 AAH19800	AAH19800 Candida a
9	16	6.1	16	7 ADC73274	ADC73274 Yeast int
10	15	5.7	15	7 ADC73269	ADC73269 Yeast int
11	15	5.7	15	7 ADC73269	ADC73269 Yeast int
12	10	3.8	58	4 ABB68460	ABB68460 Drosophill
13	10	3.8	60	4 ABB68465	ABB68465 Drosophill
14	10	3.8	99	3 ABB32604	ABB32604 Eucalyptu
15	10	3.8	286	5 AAB30808	AAB30808 Amino aci
16	10	3.8	286	5 AAB30808	AAB30808 Amino aci
17	10	3.8	333	4 ABB68754	ABB68754 Drosophill
18	10	3.8	363	5 ABB57165	ABB57165 Mouse fac
19	10	3.8	406	8 ADN20494	ADN20494 Bacteri
20	10	3.8	550	4 ABB59194	ABB59194 Drosophill
21	10	3.8	578	4 ABB58393	ABB58393 Drosophill
22	10	3.8	582	4 ABB71745	ABB71745 Drosophill
23	10	3.8	588	8 ADR48570	ADR48570 Protein a
24	10	3.8	675	4 ABB62402	ABB62402 Drosophill
25	10	3.8	717	4 ABB71958	ABB71958 Drosophill

26	10	3.8	738	7 ADK63388	ADK63388 Disease c
27	10	3.8	743	5 ABB79410	ABB79410 Candida a
28	10	3.8	743	5 ABB47970	ABB47970 Candida a
29	10	3.8	797	5 ABB64072	ABB64072 Drosophill
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31	10	3.8	900	4 ABB62018	ABB62018 Drosophill
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33	10	3.8	926	4 ABB65135	ABB65135 Drosophill
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45	10	3.8	1368	4 ABB60262	ABB60262 Drosophill
46	10	3.8	1419	4 ABB65521	ABB65521 Drosophill
47	10	3.8	1665	4 ABB64010	ABB64010 Drosophill
48	10	3.8	1692	4 AAU03390	AAU03390 Fusarium
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51	10	3.8	1798	4 ABB71695	ABB71695 Drosophill
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54	10	3.8	2439	4 ABB68896	ABB68896 Drosophill
55	10	3.8	2703	4 ABB63239	ABB63239 Drosophill
56	10	3.8	2703	5 ABB70019	ABB70019 Larval v4
57	10	3.8	3080	4 ABB64877	ABB64877 Drosophill
58	10	3.4	53	4 ABB69858	ABB69858 Drosophill
59	9	3.4	104	4 ABB67522	ABB67522 Drosophill
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61	9	3.4	198	4 ABB71093	ABB71093 Drosophill
62	9	3.4	224	4 ABB68522	ABB68522 Drosophill
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73	9	3.4	351	8 ADR15666	ADR15666 Kinase 61
74	9	3.4	353	3 AAB54362	AAB54362 Human pan
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96	9	3.4	1778	4 ABB66081	ABB66081 Drosophill
97	9	3.4	1954	4 ABB59197	ABB59197 Drosophill
98	9	3.4	2017	6 ABB54584	ABB54584 Human NOV

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OM protein - protein search, using sw model

Run on: June 8, 2005, 15:52:45 ; Search time 174 Seconds
(without alignments)
774.005 Million cell updates/sec

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Title:      US-09-964-858A-1_COPY_1_263
Perfect score: 1386
Sequence:   1 MNSTPSKLLPIDKSHSLQLQ.....NKNNEVNSPEALTTDMKLKR 263

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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: uniprot_sprot:*
2: uniprot_trembl:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

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2	384.5	27.7	1662	2	06B680	06B680 debaryomyces
3	158.5	11.2	1709	2	095PM5	095PM5 dictyostelium
4	155	11.2	1259	2	0869X4	0869X4 dictyostelium
5	148	10.7	971	1	CLAA_CANNAL	014427 candida alb
6	147	10.6	1729	1	078CT4	078CT4 neurospora
7	146	10.5	542	2	0966T0	0966T0 dictyostelium
8	145.5	10.5	2454	2	086B02	086B02 dictyostelium
9	144	10.4	2625	2	08MMZ9	08MMZ9 dictyostelium
10	143.5	10.4	1721	2	08SS00	08SS00 dictyostelium
11	142.5	10.3	687	2	06BH38	06BH38 debaryomyces
12	142.5	10.3	2678	2	09ND54	09ND54 dictyostelium
13	142	10.2	656	2	07KWS5	07KWS5 dictyostelium
14	142	10.2	2843	2	096J15	096J15 dictyostelium
15	141.5	10.2	236	1	LIPB_MYCPU	091896 mycoplasma
16	141.5	10.2	.930	2	086B39	086B39 dictyostelium
17	140.5	10.1	1502	2	08I910	08I910 dictyostelium
18	140	10.1	670	2	06BPT1	06BPT1 parametium
19	139.5	10.1	727	2	08BK34	08BK34 dictyostelium
20	138.5	10.0	1166	2	086489	086489 staphylococcus
21	138	10.0	1141	2	08NXX5	08NXX5 staphylococcus
22	137	10.0	1141	2	06GB84	06GB84 staphylococcus
23	137	9.9	730	2	08T867	08T867 dictyostelium
24	137	9.9	947	2	015739	015739 dictyostelium
25	137	9.9	1173	2	08IQ06	08IQ06 drosophila
26	136.5	9.8	927	2	07YYD8	07YYD8 cryptosporidium
27	136	9.8	593	2	08SSP5	08SSP5 dictyostelium
28	135.5	9.8	2472	2	08KMX1	08KMX1 dictyostelium
29	135	9.7	573	2	06C951	06C951 yarrowia
30	135	9.7	1008	2	06BHZ3	06BHZ3 debaryomyces
31	134.5	9.7	1137	2	06GJN6	06GJN6 staphylococcus

[illegible]

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34	134	9.7	1171	2	Q932F7	.0932f7	staphylococcus
35	134	9.7	1141	2	Q96946	.096w46	staphylococcus
36	133.5	9.6	800	2	Q96902	.096902	dictyostell
37	133	9.6	638	2	Q9V9Z6	.09v9z6	dictyostella
38	132	9.5	499	1	WETA_PENCH	.09w870	dictyostella
39	132	9.5	714	2	Q87210	.08t210	dictyostella
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42	131.5	9.5	1179	2	Q91198	.091198	white spot
43	131.5	9.5	1180	2	Q8VAS9	.08vas9	white spot
44	131.5	9.5	2267	2	Q9VMS2	.09vms2	dictyostella
45	130.5	9.4	1004	2	Q8WMP6	.08wmp6	dictyostella

ALIGNMENTS

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: June 8, 2005, 16:10:16 ; Search time 158 Seconds
(without alignments)
638.082 Million cell updates/sec

Title: US-09-964-858a-1_COPY_1_263
Perfect score: 1386
Sequence: 1 NWSTPSKLLPIDKSHSLDLO.....NNNNVNSPPALTMKLR 263

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1710399 seqs, 383334425 residues

Total number of hits satisfying chosen parameters: 1710399

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Published Applications AA:
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22: /cgn2_6/ptodata/2/pubppa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1386	100.0	1664	US-09-978-343-2	Sequence 2, Appl1
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3	1386	100.0	1664	US-09-978-343-1	Sequence 0, Appl1
4	139.5	10.1	1166	US-10-470-048B-153	Sequence 153, Appl1
5	138.5	10.0	1166	US-10-744-672-7	Sequence 7, Appl1
6	138.5	10.0	1166	US-10-744-616-7	Sequence 512, Appl1
7	137.5	9.9	1138	US-10-451-467A-512	Sequence 194, Appl1
8	134.5	9.7	1138	US-10-074-475-194	Sequence 70251, A
9	134	9.7	1141	US-10-282-122A-70251	Sequence 8, Appl1
10	133	9.6	971	US-10-093-524-8	Sequence 25, Appl1
11	128	9.2	618	US-10-655-799-25	

12	127.5	9.2	1335	US-10-470-048B-278	Sequence 278, Appl1
13	124	8.9	2781	US-10-263-929-122	Sequence 122, Appl1
14	124	8.9	2781	US-10-723-860-1472	Sequence 1472, Appl1
15	123	8.9	1080	US-10-451-467A-466	Sequence 466, Appl1
16	123	8.9	1139	US-09-820-843A-15	Sequence 15, Appl1
17	123	8.9	1139	US-10-282-122A-63564	Sequence 63564, A
18	123	8.9	1616	US-09-820-843A-16	Sequence 16, Appl1
19	123	8.9	1616	US-10-282-122A-63593	Sequence 63593, A
20	123	8.9	4019	US-09-738-973-425	Sequence 425, Appl1
21	123	8.9	4019	US-09-854-133-425	Sequence 425, Appl1
22	123	8.9	4019	US-10-144-649A-425	Sequence 425, Appl1
23	122.5	8.8	5342	US-10-425-114-72709	Sequence 72709, A
24	122.5	8.8	5342	US-10-732-923-12952	Sequence 8729, Appl1
25	121.5	8.8	6642	US-10-369-493-5013	Sequence 5013, Appl1
26	121	8.7	605	US-09-801-368-428	Sequence 428, Appl1
27	121	8.7	605	US-10-369-493-22016	Sequence 22016, A
28	121	8.7	619	US-10-470-048B-61	Sequence 61, Appl1
29	121	8.7	1213	US-10-732-923-12952	Sequence 12952, A
30	120.5	8.7	608	US-10-732-923-10720	Sequence 10720, A
31	120	8.7	844	US-09-815-242-11497	Sequence 11497, A
32	120	8.7	844	US-10-335-977-5799	Sequence 5799, Appl1
33	120	8.7	847	US-10-335-977-5800	Sequence 5800, Appl1
34	120	8.7	849	US-10-335-977-5801	Sequence 5801, Appl1
35	119.5	8.6	599	US-10-335-977-5801	Sequence 63567, A
36	119	8.6	1381	US-10-032-585-7784	Sequence 7784, Appl1
37	119	8.6	1381	US-10-451-467A-425	Sequence 425, Appl1
38	119	8.6	1920	US-10-282-122A-71413	Sequence 71413, A
39	118	8.5	460	US-10-767-701-42484	Sequence 42484, A
40	118	8.5	842	US-10-369-493-1940	Sequence 1940, Appl1
41	118	8.5	1024	US-10-479-546-1	Sequence 12, Appl1
42	118	8.5	1153	US-10-479-546-1	Sequence 1, Appl1
43	118	8.5	6641	US-10-282-122A-70580	Sequence 70580, A
44	118	8.5	10203	US-10-661-809-23	Sequence 23, Appl1
45	117.5	8.5	1274	US-10-282-122A-43837	Sequence 43837, A

ALIGNMENTS

RESULT 1

US-09-978-343-2
Sequence 2, Application US/09978343
Publication No. US20030082680A1

GENERAL INFORMATION:

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GALE, CHERYL A.
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TAN, NIAN-JUN

KENDRICK, KATHLEEN
KENDRICK, KATHLEEN

TITLE OF INVENTION: CANDIDATE ALBICANS GENE, INTEGRIN-LIKE
PROTEIN, ANTIBODIES, AND METHODS OF USE

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESS: MURTING, RALPH, GERHARDT & SCHWAPPACH, P.A.

STREET: 119 NORTH FOURTH STREET, SUITE 203

CITY: MINNEAPOLIS

STATE: MINNESOTA

COUNTRY: USA

ZIP: 55401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/978,343

FILING DATE: 15-Oct-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 06/642,846

FILING DATE: 03-MAY-1996

ATTORNEY/AGENT INFORMATION:

NAME: MURTING, ANN M.